Amendments to The Claims

The following listing of claims replaces all prior versions and listings of the claims in this application.

Listing of the Claims

1-193. (Cancelled)

194. (Currently amended) A method for identifying a compound that potentially ~~elicits or~~ modulates T1R1/T1R3 (umami) receptor-associated taste in a subject comprising:

(i) screening one or more compounds in a functional assay that detects compounds ~~which activate the T1R1/T1R3 receptor or~~ which modulate (enhance or inhibit) the ~~activation~~ activity of the T1R1/T1R3 receptor by another compound; and

(ii) identifying compounds that potentially ~~elicit or~~ modulate T1R1/T1R3 (umami) receptor-associated taste based on their ~~(a) activation of the T1R1/T1R3 (umami) taste receptor or (b)~~ modulation (enhancement or inhibition) of the ~~activation~~ activity of the T1R1/T1R3 (umami) taste receptor by another compound, wherein said T1R1 is a T1R1 polypeptide and is (i) encoded by a nucleic acid sequence comprising SEQ. ID. NO: 8, (ii) encoded by a nucleic acid sequence comprising a nucleic acid that hybridizes to SEQ. ID. NO: 8 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS, or (iii) a T1R1 polypeptide possessing at least 95% sequence identity to the T1R1 polypeptide of SEQ. ID. NO: 5;

and wherein said T1R3 is a T1R3 polypeptide and is (i) encoded by a nucleic acid sequence comprising SEQ. ID. NO: 9 or SEQ. ID. NO: 11; (ii) encoded by a nucleic acid sequence that hybridizes to SEQ. ID. NO: 9 or SEQ. ID. NO: 11 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, 10% SDS; and washing at 65°C in a solution comprising 0.2X SCC and 0.1% SDS, or (iii) a T1R3 polypeptide possessing at least 95% sequence identity to the T1R3 polypeptide of SEQ. ID. NO: 4 or SEQ. ID. NO: 7.

195. (Previously presented) The method of claim 194 wherein said T1R1 receptor is selected from the group consisting of rat T1R1, mouse T1R1 and human T1R1 and said T1R3 receptor is selected from the group consisting of rat T1R3, mouse T1R3 and human T1R3.

196. (Previously presented) The method of claim 194 wherein said T1R1 and T1R3 are of the same species origin.

197. (Previously presented) The method of claim 194 wherein said T1R1 and T1R3 are of different species origin.

198. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide ~~having~~ comprising the amino acid sequence ~~contained in~~ of SEQ. ID. NO: 5.

199. (Canceled) ~~The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 5.~~

200. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 95% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID NO: 5.

201. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 96% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID NO: 5.

202. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 97% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID NO: 5.

203. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 98% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID NO: 5.

204. (Currently amended) The method of claim 194 wherein said T1R1 is a human T1R1 polypeptide that exhibits at least 99% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID NO: 5.

205. (Currently amended) The method of claim 194 wherein said T1R1 is encoded by the ~~nutrie~~ nucleic acid sequence ~~contained in~~ of SEQ. ID. NO: 8.

206. (Currently amended) The method of claim 194 which said T1R1 is encoded by a ~~nutrie~~ nucleic acid sequence that ~~hybridizes under stringent hybridization conditions to the nucleic acid sequence contained in SEQ. ID. NO: 8~~ hybridizes to SEQ. ID. NO: 8 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

207. (Canceled) ~~The method of claim 194 wherein said T1R1 is a fragment of the polypeptide encoded by SEQ ID. NO: 8 that when expressed in association with a T1R3 polypeptide yields a T1R1/T1R3 taste receptor that is activated by umami taste stimuli.~~

208. (Canceled) ~~The method of claim 194 wherein said T1R1 comprises a fragment of the human T1R1 polypeptide contained in SEQ. ID. NO. 5 that when expressed in association with T1R3 polypeptide results in a heteromeric T1R1/T1R3 taste receptor that is activated by umami taste stimuli.~~

209. (Currently amended) The method of claim 194 wherein said T1R3 is a human T1R3 polypeptide ~~having~~ comprising the amino acid sequence ~~contained in~~ of SEQ. ID. NO: 7.

210. (Canceled) ~~The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 90% sequence identity to the polypeptide contained in of SEQ. ID. NO: 7.~~

211. (Currently amended) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 95% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID. NO: 7.

212. (Currently amended) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 96% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID. NO: 7.

213. (Currently amended) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 97% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID. NO: 7.

214. (Currently amended) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 98% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID. NO: 7.

215. (Currently amended) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 99% sequence identity to the polypeptide ~~contained in~~ of SEQ. ID. NO: 7.

216. (Currently amended) The method of claim 194 which said T1R3 is a rat T1R3 polypeptide ~~having~~ comprising the sequence ~~contained in~~ of SEQ. ID. NO: [[9]] 4.

217. (Currently amended) The method of claim 194 which said T1R3 is encoded by the nucleic acid sequence ~~contained in~~ of SEQ ID. NO: 9 or SEQ. ID. NO: 11.

218. (Currently amended) The method of claim 194 wherein said T1R3 is encoded by a nucleic acid sequence that ~~hybridizes to the nucleic acid sequence contained in SEQ. ID. NO: 9 under stringent hybridization conditions~~ hybridizes to SEQ. ID. NO: 9 or SEQ. ID. NO: 11 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS ~~or hybridizes to a fragment thereof that when expressed in association with a T1R1 polypeptide results in a heteromeric T1R1/T1R3 (umami) taste receptor that responds to umami taste stimuli~~.

219. (Previously presented) The method of claim 194 wherein said T1R1 and T1R3 sequences are expressed in a cell.

220. (Previously presented) The method of claim 194 wherein said cell is intact or permeabilized.

221. (Currently amended) The method of claim 194 wherein a membrane extract comprises said T1R1/T1R3 receptor ~~is comprised in a membrane extract~~.

222. (Previously presented) The method of claim 219 wherein said T1R1 and T1R3 receptor sequences are expressed on the surface of said cell.

223. (Previously presented) The method of claim 219 wherein the cell is a eukaryotic cell.

224. (Previously presented) The method of claim 219 wherein the cell is a prokaryotic cell.

225. (Currently amended) The method of claim 223 wherein the ~~eukaryote~~ eukaryotic cell is a yeast, insect, amphibian or mammalian cell.

226. (Currently amended) The method of claim ~~224~~ 223 wherein the cell is a CHO cell, COS cell, HEK-293 cell or Xenopus oocyte.

227. (Previously presented) The method of claim 219 wherein the cell further expresses a G protein.

228. (Previously presented) The method of claim 227 wherein said G protein is G_{a15}, G_{a16} or gustducin.

229. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on phosphorylation of said T1R1/T1R3 receptors.

230. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on the internalization of said T1R1/T1R3 receptors.

231. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on arrestin translocation.

232. (Previously presented) The method of claim 194 wherein said functional assay detects the effect on said compound on second messengers.

233. (Previously presented) The method of claim 232 wherein said second messenger is cAMP, cGMP or IP3.

234. (Previously presented) The method of claim 194 wherein said functional assay detects changes in voltage or intracellular calcium.

235. (Previously presented) The method of claim 234 wherein said functional assay includes the use of a voltage-sensitive or calcium-sensitive dye.

236. (Previously presented) The method of claim 194 wherein the functional assay detects the effect of said compound on G protein activation by said T1R1/T1R3 receptor.

237. (Previously presented) The method of claim 194 wherein said T1R1 and T1R3 sequences are linked to a reporter gene.

238. (Previously presented) The method of claim 237 wherein said reporter gene luciferase, alkaline phosphatase, or Beta-galactosidase.

239. (Currently amended) The method of claim 194 wherein a synthetic compound library comprises said one or more compounds ~~are comprised in a combinatorial chemical library~~.

240. (Currently amended) The method of claim 194 wherein a combinatorial compound library comprises said one or more compounds ~~are comprised in a peptide library~~.

241. (Previously presented) The method of claim 194 wherein said one or more compounds are compounded in a randomized library of small molecules.

242. (Currently amended) The method of claim 194 wherein said method is a high-throughout the screening method.

243. (Currently amended) The method of claim 194 wherein the functional assay screens for compounds that enhance or inhibit the ~~activation~~ activity of the T1R1/T1R3 umami taste receptor by L- glutamate.

244. (Previously presented) The method of claim 194 wherein the functional assay screens for compounds that enhance or inhibit the binding of IMP, GMP or an analog thereof to the T1R1/T1R3 umami taste receptor.

245. (Previously presented) The method of claim 194 wherein the functional assay screens for compounds that modulate inhibition of the T1R1/T1R3 umami taste receptor activity by lactisole.

246. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on signal transduction.

247. (Previously presented) The method of claim 194 wherein said functional assay detects changes in cellular polarization.

248. (Previously presented) The method of claim 247 wherein said changes are detected by voltage-clamp or patch-clamp technique.

249. (Previously presented) The method of claim 194 wherein the functional $GTP\gamma^{35}S$ assay.

250. (Previously presented) The method of claim 194 wherein said assay is a fluorescent polarization or FRET assay.

251. (Previously presented) The method of claim 194 wherein said assay detects changes in adenylate cyclase activity.

252. (Currently amended) The method of claim 194 wherein said functional assay detects the effect of said compound on ligand-specific coupling of said T1R1/T1R3 receptor with a G protein.

253. (Previously presented) The method of claim 194 wherein said functional assay detects the effects of said compound on a transmitter or hormone release.

254. (Previously presented) The method of claim 194 wherein said T1R1/T1R3 taste receptor is stably expressed by a cell.

255. (Previously presented) The method of claim 194 wherein said T1R1/T1R3 taste receptor is transiently expressed by a cell.

256. (Previously presented) The method of which 194 wherein said T1R1 and T1R3 sequences are expressed under the control of an inducible promoter.

257. (New) A method for identifying a compound that potentially modulates T1R1/T1R3 (umami) receptor-associated taste in a subject comprising:

(i) screening one or more compounds in a functional assay that detects compounds which modulate (enhance or inhibit) the activity of the T1R1/T1R3 receptor by another compound; and

(ii) identifying compounds that potentially modulate T1R1/T1R3 (umami) receptor-associated taste based on their modulation (enhancement or inhibition) of the activity of the T1R1/T1R3 (umami) taste receptor by another compound, wherein said T1R1 is a T1R1 polypeptide possessing at least 95% sequence identity to the human, mouse, or rat T1R1 of Figure 1; and wherein said T1R3 is a T1R3 polypeptide possessing at least 95% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

258. (New) The cell of claim 257 wherein said T1R1 and T1R3 are derived from different species.

259. (New) The method of claim 257 wherein said T1R1 and T1R3 are of the same species.

260. (New) The cell of claim 257 wherein T1R1 polypeptide is the human, mouse, or rat T1R1 of Figure 1.

261. (New) The cell of claim 257 wherein said T1R1 polypeptide has at least 95% sequence identity to the human, mouse, or rat T1R1 of Figure 1.

262. (New) The cell of claim 257 wherein said T1R1 polypeptide has at least 96% sequence identity to the human, mouse, or rat T1R1 of Figure 1.

263. (New) The cell of claim 257 wherein said T1R1 polypeptide has at least 97% sequence identity to the human, mouse, or rat T1R1 of Figure 1.

264. (New) The cell of claim 257 wherein said T1R1 polypeptide has at least 98% sequence identity to the human, mouse, or rat T1R1 of Figure 1.

265. (New) The cell of claim 257 wherein said T1R1 polypeptide has at least 99% sequence identity to the human, mouse, or rat T1R1 of Figure 1.

266. (New) The cell of claim 257 wherein T1R3 polypeptide is the human, mouse, or rat T1R3 of Figure 1.

267. (New) The cell of claim 257 wherein said T1R3 polypeptide has at least 95% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

268. (New) The cell of claim 257 wherein said T1R3 polypeptide has at least 96% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

269. (New) The cell of claim 257 wherein said T1R3 polypeptide has at least 97% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

270. (New) The cell of claim 257 wherein said T1R3 polypeptide has at least 98% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

271. (New) The cell of claim 257 wherein said T1R3 polypeptide has at least 99% sequence identity to the human, mouse, or rat T1R3 of Figure 1.

272. (New) The method of claim 257 wherein said T1R1 and T1R3 sequences are expressed in a cell.

273. (New) The method of claim 257 wherein said cell is intact or permeabilized.

274. (New) The method of claim 257 wherein a membrane extract comprises said T1R1/T1R3 receptor.

275. (New) The method of claim 272 wherein said T1R1 and T1R3 receptor sequences are expressed on the surface of said cell.

276. (New) The method of claim 272 wherein the cell is a eukaryotic cell.

277. (New) The method of claim 272 wherein the cell is a prokaryotic cell.

278. (New) The method of claim 276 wherein the eukaryotic cell is a yeast, insect, amphibian or mammalian cell.

279. (New) The method of claim 276 wherein the cell is a CHO cell, COS cell, HEK-293 cell or Xenopus oocyte.

280. (New) The method of claim 272 wherein the cell further expresses a G protein.

281. (New) The method of claim 280 wherein said G protein is G_{a15}, G_{a16} or gustducin.

282. (New) The method of claim 257 wherein said functional assay detects the effect of said compound on phosphorylation of said T1R1/T1R3 receptors.

283. (New) The method of claim 257 wherein said functional assay detects the effect of said compound on the internalization of said T1R1/T1R3 receptors.

284. (New) The method of claim 257 wherein said functional assay detects the effect of said compound on arrestin translocation.

285. (New) The method of claim 257 wherein said functional assay detects the effect on said compound on second messengers.

286. (New) The method of claim 285 wherein said second messenger is cAMP, cGMP or IP3.

287. (New) The method of claim 257 wherein said functional assay detects changes in voltage or intracellular calcium.

288. (New) The method of claim 287 wherein said functional assay includes the use of a voltage-sensitive or calcium-sensitive dye.

289. (New) The method of claim 257 wherein the functional assay detects the effect of said compound on G protein activation by said T1R1/T1R3 receptor.

290. (New) The method of claim 257 wherein said T1R1 and T1R3 sequences are linked to a reporter gene.

291. (New) The method of claim 290 wherein said reporter gene luciferase, alkaline phosphatase, or Beta-galactosidase.

292. (New) The method of claim 257 wherein a synthetic compound library comprises said one or more compounds.

293. (New) The method of claim 257 wherein a combinatorial compound library comprises said one or more compounds.

294. (New) The method of claim 257 wherein said one or more compounds are compounded in a randomized library of small molecules.

295. (New) The method of claim 257 wherein is a high-throughout the screening method.

296. (New) The method of claim 257 wherein the functional assay screens for compounds that enhance or inhibit the activity of the T1R1/T1R3 umami taste receptor by L-glutamate.

297. (New) The method of claim 257 wherein the functional assay screens for compounds that enhance or inhibit the binding of IMP, GMP or an analog thereof to the T1R1/T1R3 umami taste receptor.

298. (New) The method of claim 257 wherein the functional assay screens for compounds that modulate inhibition of the T1R1/T1R3 umami taste receptor activity by lactisole.

299. (New) The method of claim 257 wherein said functional assay detects the effect of said compound on signal transduction.

300. (New) The method of claim 257 wherein said functional assay detects changes in cellular polarization.

301. (New) The method of claim 300 wherein said changes are detected by voltage-clamp or patch-clamp technique.

302. (New) The method of claim 257 wherein the functional GTPγ^{35}S assay.

303. (New) The method of claim 257 wherein said assay is a fluorescent polarization or FRET assay.

304. (New) The method of claim 257 wherein said assay detects changes in adenylate cyclase activity.

305. (New) The method of claim 257 wherein said functional assay detects the effect of said compound on ligand specific coupling of said T1R1/T1R3 receptor with a G protein.

306. (New) The method of claim 257 wherein said functional assay detects the effects of said compound on a transmitter or hormone release.

307. (New) The method of claim 257 wherein said T1R1/T1R3 taste receptor is stably expressed by a cell.

308. (New) The method of claim 257 wherein said T1R1/T1R3 taste receptor is transiently expressed by a cell.

309. (New) The method of which 257 wherein said T1R1 and T1R3 sequences are expressed under the control of an inducible promoter.